

Query= SEQ ID NO:43  
(1650 letters)

| Sequences producing significant alignments: | Score<br>(bits) | E<br>Value |
|---|-----------------|------------|
| AC018552.5.95189.106311                     | 569             | e-159      |
| AC018552.5.17437.94328                      | 297             | 1e-77      |

>AC018552.5.95189.106311  
Length = 11123

Score = 569 bits (287), Expect = e-159  
Identities = 287/287 (100%)  
Strand = Plus / Plus

Query: 1257 atgctggttccgtgaagggacaaccatgtacgccctctatatcaccgtccacgggtactt 1316  
|||||  
Sbjct: 5423 atgctggttccgtgaagggacaaccatgtacgccctctatatcaccgtccacgggtactt 5482

Query: 1317 cctcatcaccttctctttggcatggtggtcctggccctggtggtctggaagatcttcac 1376  
|||||  
Sbjct: 5483 cctcatcaccttctctttggcatggtggtcctggccctggtggtctggaagatcttcac 5542

Query: 1377 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacct 1436  
|||||  
Sbjct: 5543 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacct 5602

Query: 1437 gctgggcctctcgagcctggtgggtgtgacatgggggttggccatcttcaccccggtggg 1496  
|||||  
Sbjct: 5603 gctgggcctctcgagcctggtgggtgtgacatgggggttggccatcttcaccccggtggg 5662

Query: 1497 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 1543  
|||||  
Sbjct: 5663 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 5709

Score = 563 bits (284), Expect = e-157  
Identities = 284/284 (100%)  
Strand = Plus / Plus

Query: 880 aggctttcccgaggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 939  
|||||  
Sbjct: 3710 aggctttcccgaggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 3769

Query: 940 ggcagcctgttcctcctgaatctggccttcttgggtcaatgtggggagtggtcaaagggg 999  
|||||  
Sbjct: 3770 ggcagcctgttcctcctgaatctggccttcttgggtcaatgtggggagtggtcaaagggg 3829

Query: 1000 tctgatgctgcctgctgggcccgggggctgtcttccactacttctgctctgtgccttc 1059  
|||||  
Sbjct: 3830 tctgatgctgcctgctgggcccgggggctgtcttccactacttctgctctgtgccttc 3889

Query: 1060 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 1119  
|||||  
Sbjct: 3890 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 3949

Query: 1120 tacttcgggcactacttctgaagctgagcctgggtgggctgggg 1163  
|||||  
Sbjct: 3950 tacttcgggcactacttctgaagctgagcctgggtgggctgggg 3993

Score = 228 bits (115), Expect = 9e-57  
Identities = 115/115 (100%)  
Strand = Plus / Plus

Query: 768 gagaccaccttggaccagtccacggtgcatatcctcacacgcatctcccaggcgggctg 827  
|||||  
Sbjct: 284 gagaccaccttggaccagtccacggtgcatatcctcacacgcatctcccaggcgggctg 343

Query: 828 tggggctctccatgatcttctggccttcaccattattctttatgcctttctgagg 882  
|||||  
Sbjct: 344 tggggctctccatgatcttctggccttcaccattattctttatgcctttctgagg 398

Score = 204 bits (103), Expect = 1e-49  
Identities = 103/103 (100%)  
Strand = Plus / Plus

Query: 1539 aggtgtcttcatctgctgctggttcaccatcctttacctccaagtcagagcaccacagt 1598  
|||||  
Sbjct: 8131 aggtgtcttcatctgctgctggttcaccatcctttacctccaagtcagagcaccacagt 8190

Query: 1599 ctctctcttactgcaagattggaccaggcccaactccgcatct 1641  
|||||  
Sbjct: 8191 ctctctcttactgcaagattggaccaggcccaactccgcatct 8233

Score = 204 bits (103), Expect = 1e-49  
Identities = 103/103 (100%)  
Strand = Plus / Plus

Query: 666 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 725  
|||||  
Sbjct: 43 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 102

Query: 726 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 768  
|||||  
Sbjct: 103 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 145

Score = 188 bits (95), Expect = 8e-45  
Identities = 95/95 (100%)  
Strand = Plus / Plus

Query: 1162 ggcctgcccgcctgatgggtcatcggcactgggagtgccaacagctacggcctctacacc 1221  
|||||  
Sbjct: 4169 ggcctgcccgcctgatgggtcatcggcactgggagtgccaacagctacggcctctacacc 4228

Query: 1222 atccgtgatagggagaaccgcacctctctggagct 1256  
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Sbjct: 4229 atccgtgatagggagaaccgcacctctctggagct 4263

>AC018552.5.17437.94328  
Length = 76892

Score = 297 bits (150), Expect = 1e-77  
Identities = 150/150 (100%)  
Strand = Plus / Plus

Query: 57 aggtcaggaaaagcccaccgaagggccaagaaacacctgcctggggagcaacaacatgta 116  
|||||  
Sbjct: 68998 aggtcaggaaaagcccaccgaagggccaagaaacacctgcctggggagcaacaacatgta 69057

Query: 117 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 176  
|||||  
Sbjct: 69058 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 69117

Query: 177 cgactcctgcaatgtggaaaacttgcagag 206  
|||||  
Sbjct: 69118 cgactcctgcaatgtggaaaacttgcagag 69147

Score = 297 bits (150), Expect = 1e-77  
Identities = 150/150 (100%)  
Strand = Plus / Plus

Query: 344 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttccca 403  
|||||  
Sbjct: 73847 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttccca 73906

Query: 404 agagcctttttcgatccctgccaggcaacaggtctgtggtccgcttggccgtcaccattc 463  
|||||  
Sbjct: 73907 agagcctttttcgatccctgccaggcaacaggtctgtggtccgcttggccgtcaccattc 73966

Query: 464 tggacattggtccagggactctcttcaagg 493  
|||||  
Sbjct: 73967 tggacattggtccagggactctcttcaagg 73996

Score = 283 bits (143), Expect = 2e-73  
Identities = 143/143 (100%)  
Strand = Plus / Plus

Query: 205 agatactggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 264  
|||||  
Sbjct: 71877 agatactggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 71936

Query: 265 acgcctttcctgaaggctttggtccagaacctcagcaccaaacactgcagaagacttctat 324  
|||||  
Sbjct: 71937 acgcctttcctgaaggctttggtccagaacctcagcaccaaacactgcagaagacttctat 71996

Query: 325 ttctctctggagccctctcaggt 347  
|||||  
Sbjct: 71997 ttctctctggagccctctcaggt 72019

Score = 272 bits (137), Expect = 7e-70  
Identities = 141/142 (99%), Gaps = 1/142 (0%)  
Strand = Plus / Plus

Query: 487 ttca-aggggccccggctcggcctgggagatggcagcggcggtgtgaacaatcgcttgt 545  
|||||  
Sbjct: 74849 ttcacagggccccggctcggcctgggagatggcagcggcggtgtgaacaatcgcttgt 74908

Query: 546 gggtttgagtgtgggacaaatgcatgtcaccaagctggctgagcctctggagatcgtctt 605  
|||||  
Sbjct: 74909 gggtttgagtgtgggacaaatgcatgtcaccaagctggctgagcctctggagatcgtctt 74968

Query: 606 ctctcaccagcgaccgccccct 627  
|||||  
Sbjct: 74969 ctctcaccagcgaccgccccct 74990

Score = 119 bits (60), Expect = 6e-24  
Identities = 60/60 (100%)  
Strand = Plus / Plus

Query: 1 atggcgacgcccaggggcctgggggcccctgctcctgctcctcctgctcccgacctcaggt 60  
|||||  
Sbjct: 64026 atggcgacgcccaggggcctgggggcccctgctcctgctcctcctgctcccgacctcaggt 64085

Score = 81.8 bits (41), Expect = 1e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 628 aacatgaccctcacctgtgtattctgggatgtgactaaagg 668  
|||||  
Sbjct: 75495 aacatgaccctcacctgtgtattctgggatgtgactaaagg 75535



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Bo

Search  for 

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

default

Show: 

Send to

File

Get Subsequence

Links

1: AC018552. Homo sapiens chro...[gi:27476108]

LOCUS AC018552 152156 bp DNA linear PRI 03-JAN-2003  
 DEFINITION Homo sapiens chromosome 16 clone RP11-405F3, complete sequence.

ACCESSION AC018552

VERSION AC018552.6 GI:27476108

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 152156)

AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los  
 Alamos National Laboratory.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 152156)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (14-DEC-1999) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 152156)

AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los  
 Alamos National Laboratory.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell  
 Drive, Walnut Creek, CA 94598, USA

COMMENT On Jan 3, 2003 this sequence version replaced gi:13786352.

Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los Alamos  
 National Laboratory  
 www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.8% of Sequence;  
 Estimated Total Number of Errors is 0.2.

FEATURES

source

Location/Qualifiers

1..152156

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="16"

/clone="RP11-405F3"

BASE COUNT 37744 a 39980 c 38771 g 35661 t

ORIGIN

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61 caccttctcc ctggcattcc gtgcccgagc ctggtgtcct ctccgtggag gcactgctcg
121 ctccccctgg cctacctgga gggctctgtc tgtcccttgg cctcactcc tcccagggaa
181 agtgtctggc tgggcccac ctcactgggc ctgaggactg ctgcccttgg agtcaggggc
241 attcattcat aatatcagta tttcttgggt gcctgttcta ggcttgcac gaaatatgcc

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